

Additional file 3: Gene-expression signatures (GES) used for fuzzy cluster functional annotation.

GES name	N° genes	Reference	Statistics	Subtypes or score assignment
Sorlie's SSP	500	[1]	Nearest centroid classifier	Basal-like
Hu's SSP	306	[2]		HER2-E
Parker's SSP = PAM50	50	[3]		Luminal A Luminal B Normal breast-like
Proliferation score	72	[4]	Average expression	Continuous score
TNBCtype	2188	[5]	Nearest centroid classifier	Basal-like 1 (BL1) Basal-like 2 (BL2) Immunomodulatory (IM) Luminal androgen receptor (LAR) Mesenchymal-like (M) Mesenchymal stem-like (MSL)
Teschendorff GES	813	[6]	Nearest centroid classifier	Cell cycle (CC) Cell cycle and immune response (CC+IR) Extracellular matrix (ECM) Immune response (IR) Steroid hormone response (SR)
VEGF profile	13	[7]	Average expression	Continuous score
Glycolysis profile	6	[7]	Average expression	Continuous score
Claudin-low	771	[8]	Nearest centroid classifier	Claudin-low No claudin-low
Rody's metagenes	153	[9]	Average expression	B lymphocytes (IgG) Cell types for presentation of intracellular antigens (MHC-I) Interferon response (Interferon) Interferon signal transduction (STAT1) Macrophages, monocyte/myeloid lineage cells (HCK) Professional antigen-presenting cells (MHC-II) T-cell (LCK)
M2/M1 GES	611	Our study	Weighted average expression	Continuous score (low score: M(IFN- γ) = macrophages (M1); high score: M(IL-4) = macrophages (M2))

SSP, single sample predictor; GES, gene-expression signature

References

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